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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/652,292

DATE: 09/21/2000  
TIME: 17:50:18

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\09212000\I652292.raw

ENTERED

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3 <110> APPLICANT: Dawson, Paul
4     Bowden, Donald
5     Fossey, Sallyanne
7 <120> TITLE OF INVENTION: GLUT10: A NOVEL GLUCOSE TRANSPORTER IN THE TYPE 2 DIABETES LINKED REGION
8     OF CHROMOSOME 20Q12-13.1
10 <130> FILE REFERENCE: 9151.11
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,292
C--> 12 <141> CURRENT FILING DATE: 2000-08-31
12 <160> NUMBER OF SEQ ID NOS: 28
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 4395
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (250)..(1875)
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30 caggggcagga gggacagagg cggggggggg ccggaaattt tgccggcggtt cagccgcgtt 180
32 gggggactccg gcggggatgg cgcgcgggc ecctcagcgc ccccagcaca cgcggagtc 240
34 cccgcgtccc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gtc tct gtg 291
35             Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val
36             1           5           10
38 tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339
39 Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
40 15          20          25          30
42 ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387
43 Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
44          35          40          45
46 cag gag ttc ctg gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc 435
47 Gln Glu Phe Leu Val Gly Ser Leu Leu Gly Ala Leu Leu Ala Ser
48          50          55          60
50 ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc 483
51 Leu Val Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
52          65          70          75
54 ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg 531
55 Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
56          80          85          90
58 gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc 579
59 Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
60 95          100         105         110
62 gcc att tcc ctc tcc atg gct tgc tgt atc tac gtg tca gag ctg 627
63 Ala Ile Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu
64          115         120         125
66 gtg ggg cca cgg cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc 675

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67 Val	Gly	Pro	Arg	Gln	Arg	Gly	Val	Leu	Val	Ser	Leu	Tyr	Glu	Ala	Gly		
68		130			135							140					
70	atc	acc	gtg	ggc	atc	ctg	ctc	tcc	tat	gcc	ctc	aac	tat	gca	ctg	gct	723
71	Ile	Thr	Val	Gly	Ile	Leu	Leu	Ser	Tyr	Aia	Leu	Asn	Tyr	Ala	Leu	Ala	
72		145				150						155					
74	ggt	acc	ccc	tgg	gga	tgg	agg	cac	atg	ttc	ggc	tgg	gcc	act	gca	cct	771
75	Gly	Thr	Pro	Trp	Gly	Trp	Arg	His	Met	Phe	Gly	Trp	Ala	Thr	Ala	Pro	
76		160			165				170								
78	gct	gtc	ctg	caa	tcc	ctc	agc	ctc	ctc	ttc	cct	gtc	gtt	ggt	aca	gat	819
79	Ala	Val	Leu	Gln	Ser	Leu	Ser	Leu	Leu	Phe	Leu	Pro	Ala	Gly	Thr	Asp	
80	175		180			185						190					
82	gag	act	gca	aca	cac	aag	gac	ctc	atc	cca	ctc	cag	gga	ggt	gag	gcc	867
83	Glu	Thr	Ala	Thr	His	Lys	Asp	Leu	Ile	Pro	Leu	Gln	Gly	Gly	Glu	Ala	
84		195			200				205								
86	ccc	aag	ctg	ggc	ccg	ggg	agg	cca	cgg	tac	tcc	ttt	ctg	gac	ctc	tcc	915
87	Pro	Lys	Leu	Gly	Pro	Gly	Arg	Pro	Arg	Tyr	Ser	Phe	Leu	Asp	Leu	Phe	
88		210			215				220								
90	agg	gca	cgc	gat	aac	atg	cga	ggc	cgg	acc	aca	gtg	ggc	ctg	ggg	ctg	963
91	Arg	Ala	Arg	Asp	Asn	Met	Arg	Gly	Arg	Thr	Thr	Val	Gly	Leu	Gly	Leu	
92		225			230			235									
94	gtg	ctc	tcc	cag	caa	cta	aca	ggg	cag	ccc	aac	gtg	ctg	tgc	tat	gcc	1011
95	Val	Leu	Phe	Gln	Leu	Thr	Gly	Gln	Pro	Asn	Val	Leu	Cys	Tyr	Ala		
96		240			245			250									
98	tcc	acc	atc	tcc	atc	gtc	gtt	ggg	ttc	cat	ggg	gga	tcc	tca	gcc	gtg	1059
99	Ser	Thr	Ile	Phe	Ser	Ser	Val	Gly	Phe	His	Gly	Gly	Ser	Ser	Ala	Val	
100	255		260			265			270								
102	ctg	gcc	tct	gtg	ggg	ctt	ggc	gca	gtg	aag	gtg	gca	gct	acc	ctg	acc	1107
103	Leu	Ala	Ser	Val	Gly	Leu	Gly	Ala	Val	Lys	Val	Ala	Ala	Thr	Leu	Thr	
104		275			280			285									
106	gcc	atg	ggg	ctg	gtg	gac	cgt	gca	ggc	cgc	agg	gct	ctg	ttg	cta	gct	1155
107	Ala	Met	Gly	Leu	Val	Asp	Arg	Ala	Gly	Arg	Arg	Aia	Leu	Leu	Ala		
108		290			295			300									
110	ggc	tgt	gcc	ctc	atg	gcc	ctg	tcc	gtc	agt	ggc	ata	ggc	ctc	gtc	agc	1203
111	Gly	Cys	Ala	Leu	Met	Ala	Leu	Ser	Vai	Ser	Gly	Ile	Gly	Leu	Val	Ser	
112		305			310			315									
114	ttt	gcc	gtg	ccc	atg	gac	tca	ggc	cca	agc	tgt	ctg	gct	gtg	ccc	aat	1251
115	Phe	Ala	Val	Pro	Met	Asp	Ser	Gly	Pro	Ser	Cys	Ieu	Ala	Val	Pro	Asn	
116		320			325			330									
118	gcc	acc	ggg	cag	aca	ggc	ctc	cct	ggg	gac	tct	ggc	ctg	ctg	cag	gac	1299
119	Ala	Thr	Gly	Gln	Thr	Gly	Leu	Pro	Gly	Asp	Ser	Gly	Leu	Leu	Gln	Asp	
120	335		340			345			350								
122	tcc	tct	cta	cct	ccc	att	cca	agg	acc	aat	gag	gac	caa	agg	gag	cca	1347
123	Ser	Ser	Leu	Pro	Pro	Ile	Pro	Arg	Thr	Asn	Glu	Asp	Gln	Arg	Glu	Pro	
124		355			360			365									
126	atc	ttg	tcc	act	gtc	aag	aaa	acc	aag	ccc	cat	ccc	aga	tct	gga	gac	1395
127	Ile	Leu	Ser	Thr	Ala	Lys	Lys	Thr	Lys	Pro	His	Pro	Arg	Ser	Gly	Asp	
128		370			375			380									
130	ccc	tca	gcc	cct	cct	cg	ctg	gcc	ctg	agc	tct	gcc	ctc	cct	ggg	ccc	1443
131	Pro	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Leu	Ser	Ala	Leu	Pro	Gly	Pro		

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307           180           185           190  
310 Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys  
311       195       200       205  
314 Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala  
315       210       215       220  
318 Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu  
319 225       230       235       240  
322 Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr  
323       245       250       255  
326 Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala  
327       260       265       270  
330 Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met  
331       275       280       285  
334 Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys  
335       290       295       300  
338 Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala  
339 305       310       315       320  
342 Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr  
343       325       330       335  
346 Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser  
347       340       345       350  
350 Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu  
351       355       360       365  
354 Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser  
355       370       375       380  
358 Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu  
359 385       390       395       400  
362 Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu  
363       405       410       415  
366 Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp  
367       420       425       430  
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371       435       440       445  
374 Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu  
375       450       455       460  
378 Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu  
379 465       470       475       480  
382 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe  
383       485       490       495  
386 Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe  
387       500       505       510  
390 Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr  
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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/652,292 DATE: 09/21/2000  
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date